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(54) **DNA fragment encoding a polypeptide having nitrile hydratase activity, a transformant containing the DNA fragment and a process for the production of amides using the transformant.**

(57) The present invention discloses the amino acid sequence and nucleotide sequence of the α - and β -subunits of two types of nitrile hydratase derived from *Rhodococcus rhodochrous* J-1. The DNA fragment encoding nitrile hydratase is inserted into an expression vector and the recombinant vector is used for transformation. The transformant contains multiple copies of the gene and can produce much higher levels of nitrile hydratase than conventionally used microorganisms.

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The present invention relates to a DNA fragment derived from *Rhodococcus rhodochrous* J-I and encoding a polypeptide having nitrile hydratase activity which hydrates nitriles to amides. The invention also relates to a recombinant DNA containing the above DNA fragment, and a transformant transformed with the recombinant DNA. The present invention further relates to a method of producing nitrile hydratase using the transformant and of amides using nitrile hydratase.

Nitrile hydratase or nitrilase is known as an enzyme that hydrates nitriles to amides. Microorganisms that produce nitrile hydratase include those belonging to the genus *Bacillus*, the genus *Bacteridium*, the genus *Micrococcus* and the genus *Brevibacterium* (See, JP-B-62-21517/1989, USP No. 4,001,081), the genus *Corynebacterium* and the genus *Nocardia* (See, JP-B-56-17918/1981, USP No. 4,248,968), the genus *Pseudomonas* (See, JP-B-59-37951/1984, USP No. 4,637,982), the genus *Rhodococcus*, the genus *Arthrobacter* and the genus *Microbacterium* (See, JP-A-61-162193/1986, EP-A-0188316), and *Rhodococcus rhodochrous* (See, JP-A-2-470/1990, EP-A-0307926).

Nitrile hydratase has been used to hydrate nitriles to amides. In the invention, microorganisms are engineered to contain multiple copies of a recombinant DNA encoding nitrile hydratase according to a recombinant DNA technology. The recombinant produces a remarkably high level of nitrile hydratase compared with conventionally used microorganisms.

The present inventors previously disclosed a DNA fragment derived from *Rhodococcus* sp. N-774 (FERM BP-1936) which also encodes a polypeptide having nitrile hydratase activity (JP-A-2-119778/1988).

In contrast, the present inventors utilizes a DNA fragment derived from *Rhodococcus rhodochrous* J-I for the production of nitrile hydratase. We isolated the gene encoding nitrile hydratase, inserted the gene into a suitable plasmid vector and transformed an appropriate host with the recombinant plasmid, thus successfully obtained the transformant producing nitrile hydratase which has high activity also on aromatic nitriles.

The present invention relates to

- (1) a DNA^(H) fragment encoding a polypeptide having nitrile hydratase activity, said polypeptide comprising the $\alpha^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 1 and the $\beta^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 2;
- (2) a DNA^(L) fragment encoding a polypeptide having nitrile hydratase activity, said polypeptide comprising the $\alpha^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 3 and the $\beta^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 4;
- (3) the DNA^(H) fragment of (1) which contains a nucleotide sequence encoding said $\alpha^{(H)}$ - and $\beta^{(H)}$ -subunits, comprising the DNA sequence of the $\alpha^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 5 and the DNA sequence of the $\beta^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 6;
- (4) the DNA^(L) fragment of (2) which contains a nucleotide sequence encoding said $\alpha^{(L)}$ - and $\beta^{(L)}$ -subunits, comprising the DNA sequence of the $\alpha^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 7 and the DNA sequence of the $\beta^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 8;
- (5) a recombinant DNA comprising the DNA^(H) or the DNA^(L) of (1)-(4) in a vector;
- (6) a transformant transformed with the recombinant DNA of (5);
- (7) a method for the production of nitrile hydratase which comprises culturing the transformant as described in (6) and recovering nitrile hydratase from the culture;
- (8) a method for the production of amides which comprises hydrating nitriles using nitrile hydratase as described in (7) to form amides; and
- (9) a method for the production of amides which comprises culturing the transformant as described in (6), and hydrating nitriles using the resultant culture, isolated bacterial cells, treated matter thereof, or a fixed material of them, to form amides.

The present invention is described in detail as follows.

The present invention is carried out by the steps (1)-(8):

(1) Isolation and Purification of Nitrile Hydratase and Partial Amino Acid Sequencing of Nitrile Hydratase

Two types of nitrile hydratase (designated as H type and L type, respectively) are isolated and purified from *Rhodococcus rhodochrous* J-I (FERM BP-1478) and the both enzymes are separated into α and β subunits using HPLC. N-Terminal amino acid sequence each of the subunits is determined and shown in the Sequence Listing by SEQ ID: Nos. 9-12.

(2) Preparation of a DNA Probe for a Nitrile Hydratase Gene

A DNA probe is prepared from JM105/pYUK121 (FERM BP-1937) as described in JP-A-2-119778/1990 due to the high degree of homology in the amino acid sequence between the nitrile hydratase β subunit of *Rhodococcus* sp. N-774 described in said Japanese Patent Official Gazette and those of *Rhodococcus rhodochrous* J-1. Plasmid pYUK121 containing nitrile hydratase gene derived from *Rhodococcus* sp. N-774 is prepared from a JM105/pYUK121 culture. pYUK121 DNA is digested with SphI and SalI. The SphI-SalI fragment contains the nitrile hydratase gene (shown in the Sequence Listing by SEQ ID: No. 13) of *Rhodococcus* sp. N-774. The DNA fragment is radiolabeled.

(3) Detection of a DNA Segment Containing a Nitrile Hydratase Gene from the Chromosome of *Rhodococcus rhodochrous* J-1

Chromosomal DNA is prepared from a *Rhodococcus rhodochrous* J-1 culture. The chromosomal DNA is digested with restriction enzymes and hybridized to the probe described in (2) using the Southern hybridization method [Southern, E.M., J. Mol. Biol. 98, 503 (1975)].

Two DNA fragments of a different length are screened.

(4) Construction of a Recombinant Plasmid

A recombinant plasmid is constructed by inserting the chromosomal DNA fragment as prepared in (3) into a plasmid vector.

(5) Transformation and Screening for a Transformant Containing the Recombinant Plasmid

Transformants are prepared using the recombinant plasmid as described in (4). The transformant containing the recombinant plasmid is selected using the probe as described in (2) according to the colony hybridization method [R. Bruce Wallace et. al., Nuc. Ac. Res. 9, 879 (1981)]. Additionally, the presence of the nitrile hydratase gene in the recombinant plasmid is confirmed using the Southern hybridization method. The plasmids thus selected are designated as pNHJ10H and pNHJ20L.

(6) Isolation and Purification of Plasmid DNA and Construction of the Restriction Map

Plasmid DNAs of pNHJ10H and pNHJ20L as prepared in (5) are isolated and purified. The restriction map of the DNAs is constructed (Fig. 1) to determine the region containing nitrile hydratase gene.

(7) DNA Sequencing

The extra segment of the inserted DNA fragment in pNHJ10H and pNHJ20L is excised using an appropriate restriction enzyme. The inserted DNA fragment is then used for sequencing. The nucleotide sequence of the DNA fragment (SEQ: ID Nos. 14, 15) reveals that it contains the sequence deduced from the amino acid sequence as described in (1).

(8) Production of Nitrile Hydratase Using the Transformant and Conversion of Nitriles to Amides

The transformant as described in (8) is cultured. The bacterial cells are mixed with nitriles, a substrate of nitrile hydratase, and amides are produced.

Rhodococcus rhodochrous J-1 was deposited with Fermentation Research Institute, Agency of Industrial Science and Technology, and was assigned the accession number FERM BP-1478. A transformant TGI/pNHJ10H containing pNHJ10H as described in (5) and a transformant TGI/pNHJ20L containing pNHJ20L as described in (5) were deposited with the above and assigned the accession number FERM BP-2777 and FERM BP-2778, respectively.

Any vectors including a plasmid vector (e.g., pAT153, pMP9, pHc624, pKC7, etc.), a phage vector (e.g., λ gt11 (Toyobo), Charon 4A (Amersham), etc.) may be used. Enzymes which may be used include SphI, SalI, EcoRI, BamHI, SacI, and the like, which are commercially available (Takara Shuzo). Various hosts may be used for transformation including but not limited to *E. coli* JM105 and *E. coli* TGI.

Culture media for the transformant are those ordinarily used in the art.

Conversion of nitriles to amides is carried out using nitrile hydratase, crude nitrile hydratase, the culture of the transformant, the isolated bacterial cells or treated matter thereof, and the like, prepared from the culture of the transformant.

Suitable nitriles in the invention include aromatic nitriles having 4-10 carbon atoms in the aromatic moiety and aliphatic nitriles having 2-6 carbon atoms, which are described in the European Patent Publication No. 0,307,926. Typical examples of the nitriles are 4-, 3- and 2-cyanopyridines, benzonitrile, 2,6-difluorobenzonitrile, 2-thiophene carbonitrile, 2-furonitrile, cyanopyrazine, acrylonitrile, methacrylonitrile, crotonitrile, acetonitrile and 3-hydroxypropionitrile.

The present invention discloses the amino acid sequence and nucleotide sequence of the α - and β -subunits of two types of nitrile hydratase derived from *Rhodococcus rhodochrous* J-1. The DNA fragment encoding nitrile hydratase is inserted into an expression vector and the recombinant vector is used for transformation. The transformant contains multiple copies of the gene and can produce much higher levels of nitrile hydratase than conventionally used microorganisms.

Fig. 1 shows restriction maps of recombinant plasmids, pNHJ10H and pNHJ20L.

The present invention is illustrated by the following Example.

The following abbreviations are used in the Example.

TE:	Tris-HCl (10 mM; pH 7.8), EDTA (1 mM, pH 8.0)
TNE:	Tris-HCl (50 mM; pH 8.0), EDTA (1 mM, pH 8.0), NaCl (50 mM)
STE:	Tris-HCl (50 mM; pH 8.0), EDTA (5 mM, pH 8.0), Sucrose (35 mM)
2xYT medium:	1.6% Trypton; 1.0% Yeast extract, 0.5% NaCl

Example

(1) Isolation and Purification of Nitrile Hydratase and Partial Amino Acid Sequencing of Nitrile Hydratase

Rhodococcus rhodochrous J-1 was cultured in a medium (3 g/l of yeast extract, 0.5 g/l of KH_2PO_4 , 0.5 g/l of K_2HPO_4 , 0.5 g/l of $\text{MgSO}_4 \cdot 4\text{H}_2\text{O}$, 0.01 g/l of CoCl_2 , and 3 g/l of crotonamide, pH 7.2) at 28°C for 80 hours. The bacterial cells were harvested. 50 g of the bacterial cells was disrupted and fractionated with ammonium sulfate. The sample was dialyzed and the dialysate was centrifuged. The supernatant was loaded on DEAE-Cellulofine chromatography, Phenyl-Sepharose chromatography, Sephadex G-150 chromatography and Octyl-Sepharose chromatography. Two fractions with enzyme activity were obtained and dialyzed. The dialysates were loaded on a high performance liquid chromatography using a reversed phase column (Senshu Pak VP-304-1251, Senshu Kagaku), and two respective subunits (α and β) were obtained. N-terminal amino acid sequence of $\alpha_1^{(H)}$, $\beta_1^{(H)}$, $\alpha_1^{(L)}$ and $\beta_1^{(L)}$ -subunits was determined using an Applied Biosystems model 470A protein sequencer. The amino acid sequences are shown in the Sequence Listing by SEQ ID: Nos. 9-12.

(2) Preparation of a DNA Probe for Nitrile Hydratase Gene

E. coli JM105 (FERM BP-1937) containing pYUK121 was cultured in 100 ml of 2xYT medium containing 50 $\mu\text{g}/\text{ml}$ of ampicillin at 30°C overnight (12 hours). The bacterial cells were harvested and TNE was added to the cells. The cell suspension was then centrifuged. 8 ml of STE and 10 mg of lysozyme were added to the pellet. The mixture was incubated at 0°C for five minutes followed by the addition of 4 ml of 0.25M EDTA. 2 ml of 10% SDS and 5 ml of 5M NaCl were then added to the mixture at room temperature. The resultant mixture was incubated at 0-4°C for three hours and then ultracentrifuged. 1/2 volume of 30% PEG 6000 was added to the supernatant. The mixture was incubated at 0-4°C overnight (12 hours) and centrifuged. TNE was added to the pellet to bring the volume to 7.5 ml and CsCl was then added to the suspension. The mixture was centrifuged to remove proteins. Then, 300-500 mg/ml of ethidium bromide was added to the supernatant. The mixture was transferred to a centrifuge tube. The tube was heat-sealed and then ultracentrifuged. cccDNA was extracted using a peristaltic pump. A bit more than equal amount of isopropyl alcohol saturated with water was added to the extract to rid of ethidium bromide. The sample was dialyzed against TE. About 3 ml of purified pYUK121 was obtained.

pYUK121 DNA was digested with SphI and Sall, resulting in a 2.07 kb DNA fragment containing a nitrile hydratase gene derived from *Rhodococcus* sp. N-774. The fragment was radiolabeled with ^{32}P to produce a probe. The nucleotide sequence of the probe is shown in the Sequence Listing by SEQ ID: No. 13.

(3) Preparation of a DNA Fragment Containing a Nitrile Hydratase Gene of Chromosome

Rhodococcus rhodochrous J-1 was cultured in 100 ml of a medium (10 g/l of glucose, 0.5 g/l of KH_2PO_4 , 0.5 g/l of K_2HPO_4 , 0.5 g/l of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 1 g/l of yeast extract, 7.5 g/l of peptone, 0.01 g/l of CoCl_2 , 7.5 g/l of urea, 1% glycine or 0.2 $\mu\text{g}/\text{ml}$ of ampicillin, 1 l of water, pH 7.2). The bacterial cells

were harvested and the pellet was washed with TNE. The pellet was then suspended in 10 ml of TE. 4 ml of 0.25M EDTA, 10-20 mg of lysozyme, 10-20 mg of achromoprotease and 10 ml of 10×SDS were added to the suspension. The suspension was incubated at 37° C for three hours. 15 ml of phenol was added to the suspension. The mixture was incubated at room temperature for 15 minutes and then centrifuged. The upper layer was removed, and 0.7 ml of 2.5M sodium acetate and diethyl ether were added to the supernatant. The mixture was centrifuged and the upper layer was discarded. Two volumes of ethanol were added to the bottom layer and DNA was removed with a glass rod. DNA was rinsed for five minutes each with TE:ethanol 2:8, 1:9, and 0:10 (v/v). DNA was then resuspended in 2-4 ml of TE (37° C). 10 µl of a mixture of RNase A and T₁ was added to the suspension and the mixture was incubated at 37° C. An equal amount of phenol was added to the mixture which was then centrifuged. More than equal amount of ether was added to the supernatant. The mixture was centrifuged again, and the upper layer was discarded and the bottom layer was saved. The bottom layer was dialyzed against 2 l of TE containing a small amount of chloroform overnight and further dialyzed against fresh TE for 3-4 hours. 4 ml of crude chromosomal DNA was obtained.

10 µl of TE, 3 µl of reaction buffer (10×) and 2 µl of SacI were added to 15 µl of crude chromosomal DNA. The mixture was incubated at 37° C for an hour and electrophoresed on an agarose gel at 60 V for three hours. The Southern hybridization of chromosomal DNA was carried out using the probe as described in (2). About 6.0 kb and 9.4 kb fragments were found to show a strong hybridization.

15 µl of chromosomal DNA was digested with SacI and electrophoresed on an agarose gel, as described above. 6.0 kb and 9.4 kb DNA fragments were cut out from the gel and taken in three volumes each of 8M NaClO₄. After solubilization, each solution was dotted on GF/C (Whatman) filter paper (6 mm in diameter). Ten drops (≈ 100 µl) of TE containing 6M NaClO₄ and then ten drops (≈ 100 µl) of 95% ethanol were added to the filter paper. The paper was air-dried for 3 minutes and placed in 0.5 ml Eppendorf tube. 40 µl of TE was added to the tube and the whole was incubated at 47° C for 30 minutes. The tube was then centrifuged. About 40 µl of the supernatant was obtained which contained 6.0 kb and 9.4 kb DNA fragments containing a nitrile hydratase gene of chromosomal DNA.

The method of inserting the 6.0 kb DNA fragment into a vector is described below. The same method is applied for the insertion of the 9.4 kb DNA fragment into a vector.

(4) Insertion of the Chromosomal DNA Fragment into a Vector

10 µl of TE, 3 µl of reaction buffer (10×) and 2 µl of SacI was added to 10 µl of pUC19. The mixture was incubated at 30° C for an hour. 2 µl of 0.25M EDTA was added to the mixture to stop the reaction. Then, 7 µl of 1M Tris-HCl (pH 9) and 3 µl of BAP (bacterial alkaline phosphatase) were added to the mixture. The mixture was incubated at 65° C for an hour. TE was then added to the mixture to make a total volume to 100 µl. The mixture was extracted 3× with an equal amount of phenol. An equal amount of ether was added to the extract. The bottom layer was removed and 10 µl of 3M sodium acetate and 250 µl of ethanol were added to the bottom layer. The mixture was incubated at -80° C for 30 minutes, centrifuged, dried, and resuspended in TE.

5 µl of pUC19 DNA thus obtained and 40 µl of the 6.0 kb DNA fragment as described in (3) were mixed. 6 µl of ligation buffer, 6 µl of ATP (6 mg/ml) and 3 µl of T4 DNA ligase were added to the mixture. The mixture was incubated at 4° C overnight (12 hours) to produce the recombinant plasmid containing the 6.0 kb DNA fragment encoding the desired enzyme in the SacI site of pUC19.

(5) Transformation and Screening of Transformants

E. coli TGI (Amersham) was inoculated into 10 ml of 2×YT medium and incubated at 37° C for 12 hours. After incubation, the resultant culture was added to fresh 2×YT medium to a concentration of 1%, and the mixture was incubated at 37° C for two hours. The culture was centrifuged and the pellet was suspended in 5 ml of cold 50 mM CaCl₂. The suspension was placed on ice for 40 minutes and then centrifuged. 0.25 ml of cold 50 mM CaCl₂ and 60 µl of the recombinant DNA as described in (4) were added to the pellet. The mixture was incubated at 0° C for 40 minutes, heat-shocked at 42° C for two minutes, placed on ice for five minutes, and added to 10 ml of 2×YT medium. The mixture was incubated at 37° C for 90 minutes with shaking, then centrifuged. The pellet was suspended in 1 ml of 2×YT medium, and two 10 µl aliquots of the suspension were plated on a 2×YT agar plate containing 50 µg/ml of ampicillin separately. The plate was incubated at 37° C. The colony grown on the plate was selected by the colony hybridization method: The colony was transferred to a nitrocellulose filter and digested. The DNA was fixed on the filter and hybridized to the probe as described in (2). The filter was autoradiographed and

a recombinant colony was selected. Additionally, the presence of a nitrile hydratase gene in the transformant was confirmed according to the Southern hybridization method.

(6) Isolation and Purification of Recombinant Plasmid and Construction of the Restriction Map of the Inserted DNA Fragments

The transformant selected as described in (5) was grown in 100 ml of 2xYT medium containing 50 µg/ml of ampicillin at 37°C overnight (12 hours). The bacterial cells were harvested and TNE was added to the cells. The cells were collected again by centrifugation, and 8 ml of STE and 10 mg of lysozyme were added to the cells. The mixture was incubated at 0°C for five minutes. 4 ml of 0.25M EDTA, 2 ml of 10% SDS (at room temperature) and 5 ml of 5M NaCl were added to the mixture. The mixture was incubated at 0-4°C for three hours, and ultracentrifuged. 1/2 volume of 30% PEG 6000 was added to the supernatant. The mixture was incubated at 0-4°C overnight (12 hours) and centrifuged again. TNE was added to the pellet to bring the volume up to 7.5 ml. CsCl was added to the suspension to rid of proteins. Then, 300-500 mg/ml of ethidium bromide was added to the supernatant and the mixture was transferred to a centrifuge tube. The tube was heat-sealed and ultracentrifuged. cccDNA was removed using a peristaltic pump. A bit more than equal amount of isopropyl alcohol saturated with water was added to cccDNA to remove ethidium bromide. The DNA sample was dialyzed against TE, resulting in about 3 ml of purified recombinant DNA. The recombinant plasmid thus obtained containing a 6.7 kb DNA fragment was designated as pNHJ10H. (The recombinant plasmid containing a 9.4 kb DNA fragment was designated as pNHJ20L).

These plasmid DNAs were digested with EcoRI, BamHI, PstI, SacI and Sall. The restriction maps were constructed and are shown in Fig. 1.

(7) DNA Sequencing

The location of a nitrile hydratase gene in the DNA fragment of pNHJ10H was determined according to the restriction map constructed and to the Southern hybridization method. An extra segment in pNHJ10H was cleaved off with PstI and Sall: The 6.0 kb DNA fragment resulted in 1.97 kb. Similarly, an extra segment in pNHJ20L was cleaved off with EcoRI and SacI: The 9.4 kb DNA fragment resulted in 1.73 kb.

These DNA fragments were sequenced by the Sanger method [Sanger, F., Science 214: 1205-1210 (1981)] using M13 phage vector. The nucleotide sequence of the 1.97 kb DNA fragment (pNHJ10H) and the 1.73 kb DNA fragment (pNHJ20L) are shown in the Sequence Listing by SEQ ID: No. 14 and SEQ ID: No. 15, respectively.

The amino acid sequence deduced from the nucleotide sequence was found fully identical to the amino acid sequence as determined in (1). The sequence analysis also revealed that the DNA fragment contained the sequence coding for the α- and β-subunits.

(8) Production of Nitrile Hydratase Using the Transformant and Conversion of Nitriles to Amides Using Nitrile Hydratase

TG1/pNHJ10H and TG1/pNHJ20L were inoculated into 10 ml of 2xYT medium containing 50 µg/ml of ampicillin and incubated at 30°C overnight (12 hours). 1 ml of the resultant culture was added to 100 ml of 2xYT medium (50 µg/ml of ampicillin, 0.1 g of CoCl₂·6H₂O/l). The mixture was incubated at 30°C for 4 hours. IPTG was added to the mixture to a final concentration of 1 mM. The mixture was incubated at 30°C for 10 hours. After harvesting the cells, the cells were suspended in 5 ml of 0.1 M phosphate buffer (pH 7.5). The suspensions were disrupted by sonification for 5 min and centrifuged at 12,000 ×g for 30 min. The resulting supernatants were used for the enzyme assay. The enzyme assay was carried out in a reaction mixture (12 ml) containing 50 mM potassium phosphate buffer (pH 7.5), 6 mM benzonitrile and an appropriate amount of the enzyme. The reaction was carried out at 20°C for 30 min and stopped by the addition of 0.2 ml 1 M HCl. The amount of benzamide formed in the reaction mixture was determined by HPLC. As a control, the mixture obtained by the same procedure as described above but from E. coli TG1 was used. The levels of nitrile hydratase activity in cell-free extracts of E. coli containing pNHJ10H and pNHJ20L were 1.75 × 10⁻³ and 6.99 × 10⁻³ units/mg, respectively, when cultured in 2xYT medium in the presence of CoCl₂ and IPTG. Benzamide was found in the reaction mixture of TG1/pNHJ10H and pNHJ20L, whereas no benzamide was found in the reaction mixture of TG1.

(1) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous*

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

 α (H)-subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

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      5      10      15
MetSerGluHisValAsnLysTyrThrGluTyrGluAlaArgThr
      20      25      30
LysAlaIleGluThrLeuLeuTyrGluArgGlyLeuIleThrPro
      35      40      45
AlaAlaValAspArgValValSerTyrTyrGluAsnGluIleGly
      50      55      60
ProMetGlyGlyAlaLysValValAlaLysSerTrpValAspPro
      65      70      75
GluTyrArgLysTrpLeuGluGluAspAlaThrAlaAlaMetAla
      80      85      90
SerLeuGlyTyrAlaGlyGluGlnAlaHisGlnIleSerAlaVal
      95      100      105
PheAsnAspSerGlnThrHisHisValValValCysThrLeuCys
      110      115      120
SerCysTyrProTrpProValLeuGlyLeuProProAlaTrpTyr
      125      130      135
LysSerMetGluTyrArgSerArgValValAlaAspProArgGly

```

1 4 0 1 4 5 1 5 0
 ValLeuLysArgAspPheGlyPheAspIleProAspGluValGlu
 1 5 5 1 6 0 1 6 5
 ValArgValTrpAspSerSerSerGluIleArgTyrIleValIle
 1 7 0 1 7 5 1 8 0
 ProGluArgProAlaGlyThrAspGlyTrpSerGluGluGluLeu
 1 8 5 1 9 0 1 9 5
 ThrLysLeuValSerArgAspSerMetIleGlyValSerAsnAla
 2 0 0
 LeuThrProGlnGluValIleVal

(2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\beta^{(H)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

5 1 0 1 5
 MetAspGlyIleHisAspThrGlyGlyMetThrGlyTyrGlyPro
 2 0 2 5 3 0
 ValProTyrGlnLysAspGluProPhePheHisTyrGluTrpGlu
 3 5 4 0 4 5
 GlyArgThrLeuSerIleLeuThrTrpMetHisLeuLysGlyIle
 5 0 5 5 6 0
 SerTrpTrpAspLysSerArgPhePheArgGluSerMetGlyAsn
 6 5 7 0 7 5
 GluAsnTyrValAsnGluIleArgAsnSerTyrTyrThrHisTrp

5 80 85 90
 LeuSerAlaAlaGluArgIleLeuValAlaAspLysIleIleThr
 95 100 105
 GluGluGluArgLysHisArgValGlnGluIleLeuGluGlyArg
 110 115 120
 10 TyrThrAspArgLysProSerArgLysPheAspProAlaGlnIle
 125 130 135
 GluLysAlaIleGluArgLeuHisGluProHisSerLeuAlaLeu
 140 145 150
 ProGlyAlaGluProSerPheSerLeuGlyAspLysIleLysVal
 15 155 160 165
 LysSerMetAsnProLeuGlyHisThrArgCysProLysTyrVal
 170 175 180
 ArgAsnLysIleGlyGluIleValAlaTyrHisGlyCysGlnIle
 185 190 195
 20 TyrProGluSerSerSerAlaGlyLeuGlyAspAspProArgPro
 200 205 210
 LeuTyrThrValAlaPheSerAlaGlnGluLeuTrpGlyAspAsp
 215 220 225
 25 GlyAsnGlyLysAspValValCysValAspLeuTrpGluProTyr
 LeuIleSerAla

30 (3) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 207 amino acids

(B) TYPE: Amino acid

40 (C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

45 (vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

50 (B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

55 α (L)-subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

5 MetThrAlaHisAsnProValGlnGlyThrLeuProArgSerAsn
 10 GluGluIleAlaAlaArgValLysAlaMetGluAlaIleLeuVal
 15 AspLysGlyLeuIleSerThrAspAlaIleAspHisMetSerSer
 20 ValTyrGluAsnGluValGlyProGlnLeuGlyAlaLysIleVal
 25 AlaArgAlaTrpValAspProGluPheLysGlnArgLeuLeuThr
 30 AspAlaThrSerAlaCysArgGluMetGlyValGlyGlyMetGln
 35 GlyGluGluMetValValLeuGluAsnThrGlyThrValHisAsn
 40 MetValValCysThrLeuCysSerCysTyrProTrpProValLeu
 45 GlyLeuProProAsnTrpTyrLysTyrProAlaTyrArgAlaArg
 50 AlaValArgAspProArgGlyValLeuAlaGluPheGlyTyrThr
 55 ProAspProAspValGluIleArgIleTrpAspSerSerAlaGlu
 60 LeuArgTyrTrpValLeuProGlnArgProAlaGlyThrGluAsn
 65 PheThrGluGluGlnLeuAlaAspLeuValThrArgAspSerLeu
 70 IleGlyValSerValProThrThrProSerLysAla

(4) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous*

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

 $\beta^{(L)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```

      5      10      15
MetAspGlyIleHisAspLeuGlyGlyArgAlaGlyLeuGlyPro
      20      25      30
IleLysProGluSerAspGluProValPheHisSerAspTrpGlu
      35      40      45
ArgSerValLeuThrMetPheProAlaMetAlaLeuAlaGlyAla
      50      55      60
PheAsnLeuAspGlnPheArgGlyAlaMetGluGlnIleProPro
      65      70      75
HisAspTyrLeuThrSerGlnTyrTyrGluHisTrpMetHisAla
      80      85      90
MetIleHisHisGlyIleGluAlaGlyIlePheAspSerAspGlu
      95      100      105
LeuAspArgArgThrGlnTyrTyrMetAspHisProAspAspThr
      110      115      120
ThrProThrArgGlnAspProGlnLeuValGluThrIleSerGln
      125      130      135
LeuIleThrHisGlyAlaAspTyrArgArgProThrAspThrGlu
      140      145      150
AlaAlaPheAlaValGlyAspLysValIleValArgSerAspAla
      155      160      165
SerProAsnThrHisThrArgArgAlaGlyTyrValArgGlyArg
      170      175      180
ValGlyGluValValAlaThrHisGlyAlaTyrValPheProAsp
      185      190      195
ThrAsnAlaLeuGlyAlaGlyGluSerProGluHisLeuTyrThr
      200      205      210
ValArgPheSerAlaThrGluLeuTrpGlyGluProAlaAlaPro
      215      220      225
AsnValValAsnHisIleAspValPheGluProTyrLeuLeuPro
Ala

```

(5) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

 $\alpha^{(H)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

```

      15      30      45
GTGAGCGAGCACGTC AATAAGTACACGGAGTACGAGGCACGTACC
      60      75      90
AAGGCGATCGAAACCTTGCTGTACGAGCGAGGGCTCATCACGCC
     105     120     135
GCCGCGGTCCGACCGAGTCGTTTCGTACTACGAGAACGAGATCGGC
     150     165     180
CCGATGGGCGGTGCCAAGGTCGTGGCCAAGTCCTGGGTGGACCCT
     195     210     225
GAGTACCGCAAGTGGCTCGAAGAGGACGCGACGGCCGCGATGGCG
     240     255     270
TCATTGGGCTATGCCGGTGAGCAGGCACACCAAATTTGGGCGGTC
     285     300     315
TTCAACGACTCCCAAACGCATCACGTGGTGGTGTGCACTCTGTGT
     330     345     360
TCGTGCTATCCGTGGCCGGTGCTTGGTCTCCCGCCCGCCTGGTAC
     375     390     405
AAGAGCATGGAGTACCGGTCCCGAGTGGTAGCGGACCCTCGTGGA
     420     435     450
GTGCTCAAGCGCGATTTTCGGTTTTCGACATCCCGATGAGGTGGAG

```

4 4 5 4 8 0 4 9 5
 GTCAGGGTTTGGGACAGCAGCTCCGAAATCCGCTACATCGTCATC
 5 5 1 0 5 2 5 5 4 0
 CCGGAACGGCCGGCCGGCACCGACGGTTGGTCCGAGGAGGAGCTG
 ACGAAGCTGGTGAGCCGGGACTCGATGATCGGTGTCAGTAATGCG
 10 5 5 5 5 7 0 5 8 5
 CTCACACCGCAGGAAGTGATCGTA
 6 0 0

(6) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 nucleic acids

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\beta^{(H)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

1 5 3 0 4 5
 ATGGATGGTATCCACGACACAGGCGGCATGACCGGATACGGACCG
 45 6 0 7 5 9 0
 GTCCCCTATCAGAAGGACGAGCCCTTCTTCCACTACGAGTGGGAG
 GGTCCGACCCTGTCAATTCTGACTTGGATGCATCTCAAGGGCATA
 50 1 0 5 1 2 0 1 3 5
 TCGTGGTGGGACAAGTCGCGGTCTTCCGGGAGTCGATGGGGAAC
 GAAAACTACGTCAACGAGATTGCGAACTCGTACTACACCCACTGG
 55 1 5 0 1 6 5 1 8 0
 CTGAGTGCGGCAGAACGTATCCTCGTCGCCGACAAGATCATCACC
 2 4 0 2 5 5 2 7 0

5 GAAGAAGAGCGAAAGCACCGTGTGCAAGAGATCCTTGAGGGTCCG
 TACACGGACAGGAAGCCGTCGCGGAAGTTCGATCCGGCCCAGATC
 10 GAGAAGGCGATCGAACGGCTTCACGAGCCCCACTCCCTAGCGCTT
 CCAGGAGCGGAGCCGAGTTTCTCTCTCGGTGACAAGATCAAAGTG
 AAGAGTATGAACCGCTGGGACACACACGGTGCCCGAAATATGTG
 15 CGGAACAAGATCGGGGAAATCGTCGCCTACCACGGCTGCCAGATC
 TATCCCGAGAGCAGCTCCGCCGGCCTCGGCGACGATCCTCGCCCCG
 20 CTCTACACGGTCGCGTTTTCCGCCCAGGAACTGTGGGGCGACGAC
 GGAAACGGGAAAGACGTAGTGTGCGTCGATCTCTGGGAACCGTAC
 25 CTGATCTCTGCC

(7) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous* J-1

(FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\alpha^{(L)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

5 ATGACCGCCCAACAATCCCGTCCAGGGCACGTTGCCACGATCGAAC
 GAGGAGATCGCCGCACGCGTGAAGGCCATGGAGGCCATCCTCGTC
 10 GACAAGGGCCTGATCTCCACCGACGCCATCGACCACATGTCTCTG
 GTCTACGAGAACGAGGTCTGCTCAACTCGGCGCCAAGATCGTC
 GCCCGCGCCTGGGTCTGATCCCGAGTTCAAGCAGCGCCTGCTCACC
 15 GACGCCACCAGCGCCTGCCGTGAAATGGGCGTGGCGGGCATGCAG
 GGCGAAGAAATGGTCTGCTGGAAAACACCGGCACGGTCCACAAC
 20 ATGGTCGTATGTACCTTGTGCTCGTGCTATCCGTGGCCGGTTCTC
 GGCCTGCCACCCAACCTGGTACAAGTACCCCGCCTACCGCGCCCGC
 25 GCTGTCCGCGACCCCGAGGTGTGCTGGCCGAATTCGGATATACC
 CCCGACCCTGACGTGAGATCCGGATATGGGACTCGAGTGCCGAA
 CTTGCTACTGGGTCTGCGCAACGCCAGCCGGCACCGAGAAC
 30 TTCACCGAAGAACAACCTGCGCGACCTCGTCAACCGCGACTCGCTC
 ATCGGCGTATCCGTCCCCACCACACCCAGCAAGGCC

(8) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous*

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\beta^{(L)}$ -subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

```

      1 5      3 0      4 5
ATGGATGGAATCCACGACCTCGGTGGCCGCGCCGGCCTGGGTCCG
      6 0      7 5      9 0
ATCAAGCCCGAATCCGATGAACCTGTTTTCCATTCCGATTGGGAG
      1 0 5      1 2 0      1 3 5
CGGTCCGTTTTTGACGATGTTCCCGGCGATGGCGCTGGCCGGCGCG
      1 5 0      1 6 5      1 8 0
TTCAATCTCGACCAGTTCCGGGGCGCGATGGAGCAGATCCCCCG
      1 9 5      2 1 0      2 2 5
CAGGACTACCTGACCTCGCAATACTACGAGCACTGGATGCACGCG
      2 4 0      2 5 5      2 7 0
ATGATCCACCACGGCATCGAGGCGGGCATCTTCGATTCCGACGAA
      2 8 5      3 0 0      3 1 5
CTCGACCGCCGCACCCAGTACTACATGGACCATCCGGACGACACG
      3 3 0      3 4 5      3 6 0
ACCCCCACGCGGCAGGATCCGCAACTGGTGGAGACGATCTCGCAA
      3 7 5      3 9 0      4 0 5
CTGATCACCACGGAGCCGATTACCGACGCCCGACCGACACCGAG
      4 2 0      4 3 5      4 5 0
GCCGCATTCCCGGTAGGCGACAAAGTCATCGTCCGGTCCGACGCC
      4 6 5      4 8 0      4 9 5
TCACCGAACACCCACACCCGCCGCGCCGGATACGTCCGCGGTCTGT
      5 1 0      5 2 5      5 4 0
GTCGGCGAAGTCGTGGCGACCCACGGCGCGTATGTCTTTCCGGAC
      5 5 5      5 7 0      5 8 5
ACCAACGCACTCGGCGCCGGCGAAAGCCCCGAACACCTGTACACC
      6 0 0      6 1 5      6 3 0
GTGCGGTTCTCGGCGACCGAGTTGTGGGGTGAACCTGCCGCCCCG
      6 4 5      6 6 0      6 7 5
AACGTCGTCAATCACATCGACGTGTTTCCAACCGTATCTGCTACCG
GCC

```

(9) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

 $\alpha^{(H)}$ -subunit: $\alpha_1^{(H)}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

Ser-Glu-His-Val-Asn-Lys-Tyr-Thr-Glu-Tyr-Glu-Ala-Arg-Thr-Lys
 Ala-Ile-Glu-Thr-Leu-Leu-Tyr-Glu-Arg-Gly-Leu

(10) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\beta^{(H)}$ -subunit: $\beta_1^{(H)}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

Met-Asp-Gly-Ile-His-Asp-Thr-Gly-Gly-Met-Thr-Gly-Tyr-Gly-Pro
Val-Pro-Tyr-Gln-Lys-Asp-Glu-Pro-Phe-Phe-His-Tyr-Glu

(11) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\alpha^{(L)}$ -subunit: $\alpha_1^{(L)}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

Thr-Ala-His-Asn-Pro⁵-Val-Gln-Gly-Thr¹⁰-Leu-Pro-Arg-?-Asn¹⁵-Glu

(12) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus rhodochrous

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

(A) OTHER INFORMATION

$\beta^{(L)}$ -subunit: $\beta_1^{(L)}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

Met-Asp-Gly-Ile⁵-His-Asp-Leu-Gly-Gly¹⁰-Arg-Ala-?-Leu¹⁵-?-Pro
Ile-Lys-Pro-Glu

(13) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2070 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: Rhodococcus sp.

(B) STRAIN: N-774 (FERM BP-1936)

(ix) FEATURES

from nucleotide No. 675 to 1295: subunit α

from nucleotide No. 1225 to 1960: subunit β

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

SphI
GCATGCTTTCCACATCTGGAACGTGATCGCCACGGACGGTGGTG
CCTACCAGATGTTGGACGGCAACGGATACGGCATGAACGCCGAAG
GTTTGTACGATCCGGAACCTGATGGCACACTTTGCTTCTCGACGCA
TTCAGCACGCCGACGCTCTGTCCGAAACCGTCAAACCTGGTGGCCC
TGACCGGCCAACACGGCATCACCCCTCGGCGGCGGAGCTACG
GCAAAGCCCGGAACCTCGTACCGCTTGCCCGCGCCGCTACGACA
CTGCCTTGAGACAATTCGACGTCCTGGTGAAGCCAACGCTGCCCT
ACGTGCGATCCGAATTGCCGGCGAAGGACGTAGATCGTGCAACCT

TCATCACCAAGGCTCTCGGGATGATCGCCAACACGGGCACCA⁴⁰⁰TTCG
 5 ACGTGACCGGACATCCGTCCCTGTCCGTTCCGGCCGGCCTGGTGA
 ACGGGGTTCCGGTCCGAATGATGATCACCGGCAGACACTT⁴⁵⁰CGACG
 ATGCGACAGTCCTTCCGTGTCCGACGCGCATTTCGAAAAGCTTCGCG⁵⁰⁰
 10 GCGGGTTTCCGACGCGCGCCGAACGCGCCTCCAACCTCTGCACCAC
 AACTCAGCCCCGCCTAGT⁵⁵⁰CTGACGCACTCTCAGACAACAAATTC
 15 CACCGATTCAACATGATCAGCC⁶⁰⁰CACATAAGAAAAGGTGAACCAG
 ATGTCAGTAACGATCGACCACACAAC⁶⁵⁰CGAGAACGCCGCACCGGCC
 MetSerValThrIleAspHisThrThrGluAsnAlaAlaProAla⁷⁰⁰
 20 Subunit α
 CAGGCGGCGGTCTCCGACCGGGCGTGGGCACTGTTCCGCGCACTC⁷⁵⁰
 GlnAlaAlaValSerAspArgAlaTrpAlaLeuPheArgAlaLeu
 Kpn I⁸⁰⁰
 25 GACGGTAAGGGATTGGTACCCGACGGTTACGTCGAGGGATGGAAG
 AspGlyLysGlyLeuValProAspGlyTyrValGluGlyTrpLys
 AAGACCTCCGAGGAGGACTTCAGTCCAAGGCGCGGAGCGGAATTG⁸⁵⁰
 LysThrSerGluGluAspPheSerProArgArgGlyAlaGluLeu
 30 Pvu II
 GTAGCGCGCGCATGGACCGACCCCGAGTTCCGGCAGCTGCTTCTC
 ValAlaArgAlaTrpThrAspProGluPheArgGlnLeuLeuLeu
 Kpn I⁹⁰⁰
 35 ACCGACGGTACCGCCGCACTTGCCCAGTACGGATACCTGGGCCCC
 ThrAspGlyThrAlaAlaValAlaGlnTyrGlyTyrLeuGlyPro
 CAGGCGGCCTACATCGTGGCAGTCGAAGACACCCCGACACTCAAG⁹⁵⁰
 GlnAlaAlaTyrIleValAlaValGluAspThrProThrLeuLys
 40 AACGTGATCGTGTGCTCGCTGTGTTTCATGCACCGCGTGGCCCATC
 AsnValIleValCysSerLeuCysSerCysThrAlaTrpProIle
 CTCGGTCTGCCACCCACCTGGTACAAGAGCTTCGAATACCGTGCG¹⁰⁰⁰
 45 LeuGlyLeuProProThrTrpTyrLysSerPheGluTyrArgAla

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5 CGCGTGGTCCGCGAACCACGGAAGGTTCTCTCCGAGATGGGAACC
 ArgValValArgGluProArgLysValLeuSerGluMetGlyThr
 GAGATCGCGTCCGACATCGAGATTCCGGTCTACGACACCACCGCC
 GluIleAlaSerAspIleGluIleArgValTyrAspThrThrAla
 10 GAAACTCGCTACATGGTCCTCCCGCAGCGTCCCGCCGGCACCGAA
 GluThrArgTyrMetValLeuProGlnArgProAlaGlyThrGlu
 Pst I
 GGCTGGAGCCAGGAACAACCTGCAGGAAATCGTCACCAAGGACTGC
 GlyTrpSerGlnGluGlnLeuGlnGluIleValThrLysAspCys
 15 CTGATCGGGGTTGCAATCCCGCAGGTTCCACCGTCTGATCACCC
 LeuIleGlyValAlaIleProGlnValProThrValTRM
 CGACAAGAAGGAAGCACACC-ATGGATGGAGTACACGATCTTGCC
 MetAspGlyValHisAspLeuAla
 Subunit β
 20 GGAGTACAAGGCTTCGGCAAAGTCCCGCATACCGTCAACGCCGAC
 GlyValGlnGlyPheGlyLysValProHisThrValAsnAlaAsp
 25 ATCGGCCCCACCTTTTCACGCCGAATGGGAACACCTGCCCTACAGC
 IleGlyProThrPheHisAlaGluTrpGluHisLeuProTyrSer
 CTGATGTTCCCGGTGTCCCGAAGTCCGGGCTTCAGCGTCGAC
 30 LeuMetPheAlaGlyValAlaGluLeuGlyAlaPheSerValAsp
 Sal I
 GAAGTGCGATACGTCTGTCGAGCGGATGGAGCCGGGCCACTACATG
 GluValArgTyrValValGluArgMetGluProGlyHisTyrMet
 35 ATGACCCCGTACTACGAGAGGTACGTCATCGGTGTGCGGACATTG
 MetThrProTyrTyrGluArgTyrValIleGlyValAlaThrLeu
 ATGGTCGAAAAGGGAATCCTGACGCAGGACGAACTCGAAAGCCTT
 40 MetValGluLysGlyIleLeuThrGlnAspGluLeuGluSerLeu
 GCGGGGGGACCGTTCCCACTGTCACGGCCAGCGAATCCGAAGGG
 AlaGlyGlyProPheProLeuSerArgProSerGluSerGluGly

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CGGCCGGCACCCGTCGAGACGACCACCTTCGAAGTCGGGGCAGCGA¹⁷⁰⁰
 ArgProAlaProValGluThrThrThrPheGluValGlyGlnArg
 5 GTACGCGTACGCGACGAGTACGTTCCGGGGCATATTTCGAATGCCT¹⁷⁵⁰
 ValArgValArgAspGluTyrValProGlyHisIleArgMetPro
 GCATACTGCCGTGGACGAGTGGGAACCATCTCTCATCGAACTACC
 10 AlaTyrCysArgGlyArgValGlyThrIleSerHisArgThrThr
 GAGAAGTGGCCGTTTCCCGACGCAATCGGGCCACGGGCGCAACGAC¹⁸⁰⁰
 GluLysTrpProPheProAspAlaIleGlyHisGlyArgAsnAsp
 GCCGGCGAAGAACCGACGTACCACGTGAAGTTCGCCGCCGAGGAA¹⁸⁵⁰
 AlaGlyGluGluProThrTyrHisValLysPheAlaAlaGluGlu
 TTGTTCGGTAGCGACACCGACGGTGGAAAGCGTCGTTGTGACCTC¹⁹⁰⁰ Sal I
 20 LeuPheGlySerAspThrAspGlyGlySerValValValAspLeu
 TTCGAGGGTTACCTCGAGCCTGCGGGCCTGATCTTCCAGCATTCCA¹⁹⁵⁰
 PheGluGlyTyrLeuGluProAlaAlaTRM
 GGCGGCGGTACGCGATCACAGCGGTTTCGTGCGACCGCCGCCTGA²⁰⁰⁰
 25 TCACCACGATTCACTCATTTCGGAAGGACACTGGAAATCATGGTTCG²⁰⁵⁰
 Sal I
 AC

(14) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1970 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous* J-1

(FERM BP-1478)

(ix) FEATURES

from nucleotide No. 408 to 1094: subunit $\beta^{(H)}$ from nucleotide No. 1111 to 1719: subunit $\alpha^{(H)}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

```

15      10      20      30      40      50      60
      CTGCAGCTCGAACATCGAAGGGTGGGAGCCGAGAGATCGGAGACGCAGACACCCGGAGGG

20      70      80      90     100     110     120
      AACTTAGCCTCCCGGACCGATGCGTGTCTTGGCAACGCCTCAAATTCAGTGCAAGCGAT

      130     140     150     160     170     180
      TCAATCTTGTTACTTCCAGAACCGAATCACGTCCCCGTAGTGTGCGGGGAGAGCGCCCGA

25      190     200     210     220     230     240
      ACGCAGGGATGGTATCCATGCGCCCCTTCTCTTTTCGAACGAGAACCGGCCGGTACAGCC

      250     260     270     280     290     300
      GACCCGGAGACACTGTGACGCCGTTCAACGATTGTTGTGCTGTGAAGGATTACCCAAGC

30      310     320     330     340     350     360
      CAACTGATATCGCCATTCCGTTGCCGGAACATTTGACACCTTCTCCCTACGAGTAGAAGC

      370     380     390     400     410     420
      CAGCTGGACCCCTCTTTGAGCCCAGCTCCGATGAAAGGAATGAGGAAATGGATGGTATCC
                                     MetAspGlylleH
                                     Subunit  $\beta^{(H)}$ 

      430     440     450     460     470     480
      ACGACACAGGCGGCATGACCGGATACGGACCGGTCCCCTATCAGAAGGACGAGCCCTTCT
40      isAspThrGlyGlyMetThrGlyTyrGlyProValProTyrGlnLysAspGluProPheP

      490     500     510     520     530     540
      TCCACTACGAGTGGGAGGGTCCGACCCTGTCAATTCTGACTTGGATGCATCTCAAGGGCA
      heHisTyrGluTrpGluGlyArgThrLeuSerIleLeuThrTrpMetHisLeuLysGlyI

      550     560     570     580     590     600
      TATCGTGGTGGGACAAGTCGCGGTTCTTCCGGGAGTCGATGGGGAACGAAACTACGTCA
45      leSerTrpTrpAspLysSerArgPhePheArgGluSerMetGlyAsnGluAsnTyrValA

      610     620     630     640     650     660
      ACGAGATTCCGCAACTCGTACTACACCCACTGGCTGAGTGCGGCAGAACGTATCCTCGTCC
      snGluIleArgAsnSerTyrThrHisTrpLeuSerAlaAlaGluArgIleLeuValA

      670     680     690     700     710     720
      CCGACAAGATCATCACCAGAAGAAGAGCGAAAGCACCGTGTGCAAGAGATCCTTGAGGGTC
50      laAspLysIlelleThrGluGluGluArgLysHisArgValGlnGluIleLeuGluGlyA

```

55

730 740 750 760 770 780
 GGTACACGGACAGGAAGCCGTCGCGGAAGTTCGATCCGGCCCAGATCGAGAAGGCGATCG
 rgTyrThrAspArgLysProSerArgLysPheAspProAlaGlnIleGluLysAlaIleG
 5 AACGGCTTCACGAGCCCCACTCCCTAGCGCTTCCAGGAGCGGAGCCGAGTTTCTCTCTCG
 luArgLeuHisGluProHisSerLeuAlaLeuProGlyAlaGluProSerPheSerLeuG
 850 860 870 880 890 900
 GTGACAAGATCAAAGTGAAGAGTATGAACCCGCTGGGACACACACGGTGCCCCGAAATATG
 lyAspLysIleLysValLysSerMetAsnProLeuGlyHisThrArgCysProLysTyrV
 10 TCGGGAACAAGATCGGGGAAATCGTCGCCTACCACGGCTGCCAGATCTATCCCGAGAGCA
 alArgAsnLysIleGlyGluIleValAlaTyrHisGlyCysGlnIleTyrProGluSerS
 910 920 930 940 950 960
 GCTCCGCCCGCTCGGCGACGATCCTCGCCCGCTCTACACGGTCGCGTTTTCCGCCCAGG
 15 erSerAlaGlyLeuGlyAspAspProArgProLeuTyrThrValAlaPheSerAlaGlnG
 970 980 990 1000 1010 1020
 AACTGTGGGGCGACGACGGAAACGGGAAAGACGTAGTGTGCGTCGATCTCTGGGAACCGT
 luLeuTrpGlyAspAspGlyAsnGlyLysAspValValCysValAspLeuTrpGluProT
 20 1030 1040 1050 1060 1070 1080
 ACCTGATCTCTGCGTGAAAGGAATACGATAGTGAGCGAGCACGTCAATAAGTACACGGAG
 yrLeuIleSerAla MetSerGluHisValAsnLysTyrThrGlu
 Subunit α (H)
 1150 1160 1170 1180 1190 1200
 25 TACGAGGCACGTACCAAGGCGATCGAAACCTTGCTGTACGAGCGAGGGCTCATCACGCC
 TyrGluAlaArgThrLysAlaIleGluThrLeuLeuTyrGluArgGlyLeuIleThrPro
 1210 1220 1230 1240 1250 1260
 GCCGCGGTGACCGAGTCGTTTCGTACTACGAGAACGAGATCGGCCCGATCGGCGGTGCC
 AlaAlaValAspArgValValSerTyrTyrGluAsnGluIleGlyProMetGlyGlyAla
 30 1270 1280 1290 1300 1310 1320
 AAGGTCGTGGCCAAGTCCTGGGTGGACCCTGAGTACCGCAAGTGGCTCGAAGAGGACGCG
 LysValValAlaLysSerTrpValAspProGluTyrArgLysTrpLeuGluGluAspAla
 1330 1340 1350 1360 1370 1380
 35 ACGGCCGCGATGGCGTCATTGGGCTATGCCGGTGAGCAGGCACACCAAATTTCCGGCGGTC
 ThrAlaAlaMetAlaSerLeuGlyTyrAlaGlyGluGlnAlaHisGlnIleSerAlaVal
 1390 1400 1410 1420 1430 1440
 TTCAACGACTCCCAAACGCATCACGTGGTGGTGTGCACTCTGTGTTTCGTGCTATCCGTGG
 PheAsnAspSerGlnThrHisHisValValValCysThrLeuCysSerCysTyrProTrp

1450 1460 1470 1480 1490 1500
 CCGGTGCTTGGTCTCCCGCCCGCCTGGTACAAGAGCATGGAGTACCGGTCCCGAGTGGTA
 ProValLeuGlyLeuProProAlaTrpTyrLysSerMetGluTyrArgSerArgValVal
 5
 1510 1520 1530 1540 1550 1560
 GCGGACCCTCGTGGAGTGCTCAAGCGCGATTTCGGTTTCGACATCCCGATGAGGTGGAG
 AlaAspProArgGlyValLeuLysArgAspPheGlyPheAspIleProAspGluValGlu
 10
 1570 1580 1590 1600 1610 1620
 GTCAGGGTTTGGGACAGCAGCTCCGAAATCCGCTACATCGTCATCCCGGAACGGCCGGCC
 ValArgValTrpAspSerSerSerGluIleArgTyrIleValIleProGluArgProAla
 1630 1640 1650 1660 1670 1680
 GGCACCGACGGTTGGTCCGAGGAGGAGCTCAGCAAGCTGGTGAGCCGGGACTCGATGATC
 GlyThrAspGlyTrpSerGluGluGluLeuThrLysLeuValSerArgAspSerMetIle
 15
 1690 1700 1710 1720 1730 1740
 GGTGTCAGTAATGCGCTCACACCGCAGGAAGTGATCGTATGAGTGAAGACACACTCACTG
 GlyValSerAsnAlaLeuThrProGlnGluValIleVal
 1750 1760 1770 1780 1790 1800
 ATCGGCTCCCGGCGACTGGGACCGCCGCACCGCCCCGCGACAATGGCGAGCTTGTATTCA
 20
 1810 1820 1830 1840 1850 1860
 CCGAGCCTTGGGAAGCAACGGCATTTCGGGGTCCGCATCGCGCTTTCGGATCAGAAGTCGT
 1870 1880 1890 1900 1910 1920
 25
 ACGAATGGGAGTTCTTCCGACAGCGTCTCATTCACTCCATCGCTGAGGCCAACGGTTGCG
 1930 1940 1950 1960 1970
 30
 AGGCATACTACGAGAGCTGGACAAAGGCGCTCGAGGCCAGCGTGGTCGAC
 35
 40

(15) INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1731 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Rhodococcus rhodochrous*

(B) STRAIN: J-1 (FERM BP-1478)

(ix) FEATURES

from nucleotide No. 171 to 848: subunit β (L)

from nucleotide No. 915 to 1535: subunit α (L)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

```

      10      20      30      40      50      60
GAGCTCCCTGGAGCCACTCGCGCCGACGCATCCACGCTCGGACAGCCACGGTGCGGATC

      70      80      90     100     110     120
ACCCCTGTTCTCGGTAACAGAACAGTAACATGTCATCAGGTCATGACCTGTTGACGCAT

      130     140     150     160     170     180
TAGACGAGGGCACATAGGGTTGGTGACTCACGGCACAAGGAGAGCATTTCATGGATGGAA
                               MetAspGlyI
                               Subunit  $\beta$  (L)

      190     200     210     220     230     240
TCCACGACCTCGGTGGCCGCGCCGGCCTGGGTCCGATCAAGCCCGAATCCGATGAACCTG
IeHisAspLeuGlyGlyArgAlaGlyLeuGlyProIleLysProGluSerAspGluProV

      250     260     270     280     290     300
TTTTCCATTCCGATTGGGAGCGGTCTGGTTTTCACGATGTTCCCGCGGATGGCGCTGGCCG
aIPheHisSerAspTrpGluArgSerValLeuThrMetPheProAlaMetAlaLeuAlaG

      310     320     330     340     350     360
GCGCGTTCAATCTCGACCAGTTCCGGGGCGCGATGGAGCAGATCCCCCGCACGACTACC
IyAlaPheAsnLeuAspGlnPheArgGlyAlaMetGluGlnIleProProHisAspTyrL

      370     380     390     400     410     420
TGACCTCGCAATACTACGAGCACTGGATGCACGCGATGATCCACCACGGCATCGAGGCGG
euThrSerGlnTyrTyrGluHisTrpMetHisAlaMetIleHisHisGlyIleGluAlaG

      430     440     450     460     470     480
GCATCTTCGATTCCGACGAACTCGACCGCGCACCCAGTACTACATGGACCATCCGGACG
IyIlePheAspSerAspGluLeuAspArgArgThrGlnTyrTyrMetAspHisProAspA

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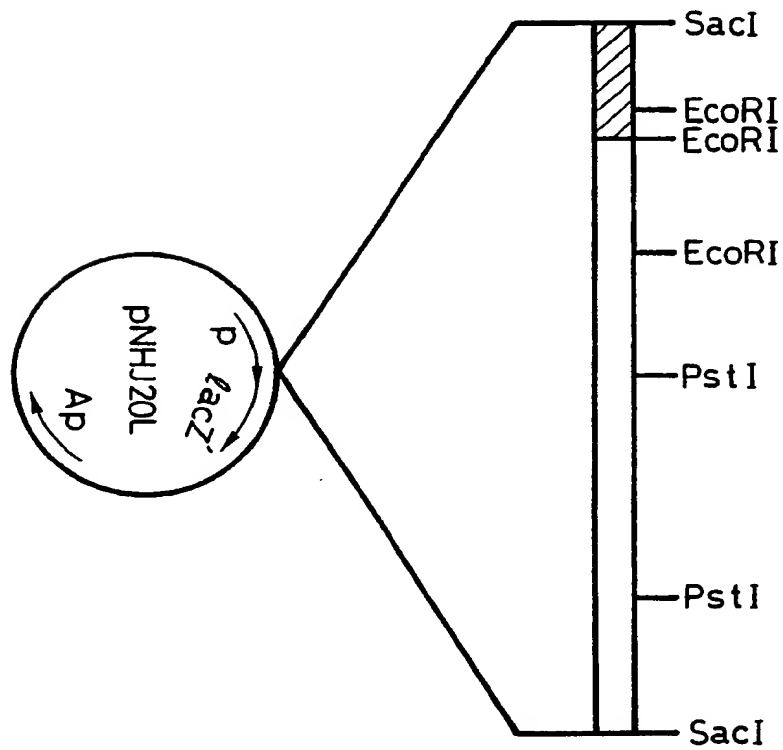
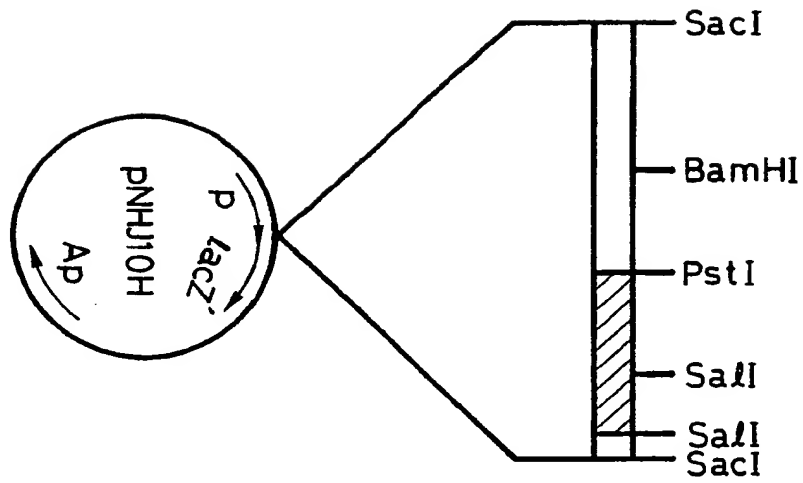
490 500 510 520 530 540
 ACACGACCCCCACGCGGCAGGATCCGCAACTGGTGGAGACGATCTCGCAACTGATCACCC
 spThrThrProThrArgGlnAspProGlnLeuValGluThrIleSerGlnLeuIleThrH
 5
 550 560 570 580 590 600
 ACGGAGCCGATTACCGACGCCCGACCGACACCGAGGCCGATTCCGCCGTAGGCGACAAAG
 isGlyAlaAspTyrArgArgProThrAspThrGluAlaAlaPheAlaValGlyAspLysV
 610 620 630 640 650 660
 10 TCATCGTGCGGTTCGGACGCCTCACCGAACACCCACACCCGCCGCCGGATACGTCCGCG
 alIleValArgSerAspAlaSerProAsnThrHisThrArgArgAlaGlyTyrValArgG
 670 680 690 700 710 720
 GTCGTGTCGGCGAAGTCGTGGCGACCCACGGCGCGTATGTCTTCCGGACACCAACGCAC
 lyArgValGlyGluValValAlaThrHisGlyAlaTyrValPheProAspThrAsnAlaL
 730 740 750 760 770 780
 15 TCGGCGCCGGCGAAAGCCCCGAACACCTGTACACCGTGCGGTTCTCGGCGACCGAGTTGT
 euGlyAlaGlyGluSerProGluHisLeuTyrThrValArgPheSerAlaThrGluLeuT
 790 800 810 820 830 840
 20 GGGGTGAACCTGCCGCCCGAACGTCGTCATCACATCGACGTGTTTCAACCGTATCTGC
 rpGlyGluProAlaAlaProAsnValValAsnHisIleAspValPheGluProTyrLeuL
 850 860 870 880 890 900
 TACCGGCCTGACCAGGTCATCCGGTCCACCCAGCGAGACGTCCCTTCACCACAGACAGAA
 euProAla
 910 920 930 940 950 960
 25 ACGAGCCACCCCGATGACCGCCCAACATCCCGTCCAGGGCACGTTGCCACGATCGAACG
 MetThrAlaHisAsnProValGlnGlyThrLeuProArgSerAsnG
 Subunit α (L)
 970 980 990 1000 1010 1020
 30 AGGAGATCGCCGCACGCGTGAAGGCCATGGAGGCCATCCTCGTCGACAAGGGCCTGATCT
 luGluIleAlaAlaArgValLysAlaMetGluAlaIleLeuValAspLysGlyLeuIleS
 1030 1040 1050 1060 1070 1080
 CCACCGACGCCATCGACCACATGTCCTCGGTCTACGAGAACCAGGTCCGTCTCAACTCG
 erThrAspAlaIleAspHisMetSerSerValTyrGluAsnGluValGlyProGlnLeuG
 1090 1100 1110 1120 1130 1140
 35 GCGCCAAGATCGTCGCCCGCGCCTGGGTTCGATCCCGAGTTCAAGCAGCGCCTGCTCACC
 lyAlaLysIleValAlaArgAlaTrpValAspProGluPheLysGlnArgLeuLeuThra
 1150 1160 1170 1180 1190 1200
 40 ACGCCACCAGCGCCTGCCGTGAAATGGGCGTCGGCGGCATGCAGGGCGAAGAAATGGTCC
 spAlaThrSerAlaCysArgGluMetGlyValGlyGlyMetGlnGlyGluGluMetValV
 1210 1220 1230 1240 1250 1260
 TGCTGGAAAACACCGGCACGGTCCACAACATGGTTCGTATGTACCTTGTGCTCGTGCTATC
 alLeuGluAsnThrGlyThrValHisAsnMetValValCysThrLeuCysSerCysTyrP
 1270 1280 1290 1300 1310 1320
 45 CGTGGCCGGTTCTCGGCCTGCCACCCAACCTGGTACAAGTACCCCGCCTACCGCGCCCGCG
 roTrpProValLeuGlyLeuProProAsnTrpTyrLysTyrProAlaTyrArgAlaArgA
 1330 1340 1350 1360 1370 1380
 CTGTCCGCGACCCCGAGGTGTGCTGGCCGAATTCGGATATACCCCGACCTGACGTCTG
 laValArgAspProArgGlyValLeuAlaGluPheGlyTyrThrProAspProAspValG

1390 1400 1410 1420 1430 1440
 AGATCCGGATATGGGACTCGAGTGCCGAACCTTCGCTACTGGGTCCTGCCGCAACGCCAC
 5 lulleArglleTrpAspSerSerAlaGluLeuArgTyrTrpValLeuProGlnArgProA
 1450 1460 1470 1480 1490 1500
 CCGGCACCGAGAACTTCACCGAAGAACAACCTCGCCGACCTCGTCACCCGCGACTCGCTCA
 laGlyThrGluAsnPheThrGluGluGlnLeuAlaAspLeuValThrArgAspSerLeuI
 1510 1520 1530 1540 1550 1560
 10 TCGGCGTATCCGTCCCCACCCACCCAGCAAGGCCTGACATGCCCCGACTCAACGAACAA
 leGlyValSerValProThrThrProSerLysAla
 1570 1580 1590 1600 1610 1620
 CCCCACCCGGGTCTCGAAGCCAACCTCGGCGACCTGGTACAGAATCTGCCGTTCAACGAA
 1630 1640 1650 1660 1670 1680
 15 CGAATCCCCCGCGCTCCGGCGAGGTGGCCTTCGATCAGGCCTGGGAGATCCGCGCCTTC
 1690 1700 1710 1720 1730
 AGCATTGCCACCGCATTGCATGGCCAGGGCCGATTGGAATGGGACGAATTC

Claims

1. A DNA^(H) fragment encoding a polypeptide having nitrile hydratase activity, said polypeptide comprising the $\alpha^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 1 and the $\beta^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 2.
2. A DNA^(L) fragment encoding a polypeptide having nitrile hydratase activity, said polypeptide comprising the $\alpha^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 3 and the $\beta^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 4.
3. The DNA^(H) fragment of claim 1 which contains the nucleotide sequences of the $\alpha^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 5 and the $\beta^{(H)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 6.
4. The DNA^(L) fragment of claim 2 which contains the nucleotide sequences of the $\alpha^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 7 and the $\beta^{(L)}$ -subunit as defined in the Sequence Listing by SEQ ID: No. 8.
5. A recombinant DNA comprising a DNA^(H) or DNA^(L) of any one of claims 1-4 in a vector.
6. A transformant transformed with the recombinant DNA of claim 5.
7. A method of producing nitrile hydratase which comprises culturing the transformant as claimed in claim 6 and recovering nitrile hydratase from the culture.
8. A method of producing amides which comprises hydrating nitriles using nitrile hydratase obtained from the culture of the transformant of claim 6.
9. A method of producing amides which comprises culturing the transformant as claimed in claim 6, and hydrating nitriles to amides using the resultant culture, isolated bacterial cells, treated matter thereof, or a fixed material thereof.

FIG. 1



(10)



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C12P 13/02**

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(54) **DNA fragment encoding a polypeptide having nitrile hydratase activity, a transformant containing the DNA fragment and a process for the production of amides using the transformant.**

(57) The present invention discloses the amino acid sequence and nucleotide sequence of the α - and β -subunits of two types of nitrile hydratase derived from Rhodococcus rhodochrous J-1. The DNA fragment encoding nitrile hydratase is inserted into an expression vector and the recombinant vector is used for transformation. The transformant contains

multiple copies of the gene and can produce much higher levels of nitrile hydratase than conventionally used microorganisms.



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number

EP 91102937.9

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. CL.5)
D,A	<u>FR - A1 - 2 633 938</u> (TERUHIKO BEPPU et al.) * Claims * & JP-A-2-119 778 --	1,6-9	C 12 N 15/53 C 07 H 21/04 C 12 P 13/02
P,A	CHEMICAL ABSTRACTS, vol. 112, no. 13, March 26, 1990, Columbus, Ohio, USA O. IKEHATA et al. "Primary structure of nitrile hydratase deduced from the nucleotide sequence of a Rhodococcus species and its expression in Escherichia coli" page 176, right column, abstract-no. 112 972f & Eur. J. Biochem. 1989, 181 (3), 563-70 --	1	
D,A	<u>EP - A2 - 0 307 926</u> (YAMADA et al.) * Abstract * ----	1,8,9	TECHNICAL FIELDS SEARCHED (Int. CL.5) C 12 N C 07 H C 12 P
The present search report has been drawn up for all claims			
Place of search VIENNA	Date of completion of the search 28-10-1991	Examiner WOLF	
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

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